

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:

10/539,630

Source:

PCT

Date Processed by STIC:

6/30/65

ENTERED

BEST AVAILABLE COPY



PCT

RAW SEQUENCE LISTING

DATE: 06/30/2005

PATENT APPLICATION: US/10/539,630

TIME: 17:41:33

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\06302005\J539630.raw

2 <110> APPLICANT: Takeda Chemical Industries, Ltd.
 4 <120> TITLE OF INVENTION: Preventing and treating agent for cancer
 6 <130> FILE REFERENCE: 3130WO0P
 C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/539,630
 C--> 8 <141> CURRENT FILING DATE: 2005-06-17
 8 <150> PRIOR APPLICATION NUMBER: JP2002-373144
 9 <151> PRIOR FILING DATE: 2002-12-24
 11 <160> NUMBER OF SEQ ID NOS: 14
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 751
 15 <212> TYPE: PRT
 16 <213> ORGANISM: Human
 18 <400> SEQUENCE: 1
 19 Met Gly Gln Thr Gly Lys Lys Ser Glu Lys Gly Pro Val Cys Trp Arg
 20 5 10 15
 21 Lys Arg Val Lys Ser Glu Tyr Met Arg Leu Arg Gln Leu Lys Arg Phe
 22 20 25 30
 23 Arg Arg Ala Asp Glu Val Lys Ser Met Phe Ser Ser Asn Arg Gln Lys
 24 35 40 45
 25 Ile Leu Glu Arg Thr Glu Ile Leu Asn Gln Glu Trp Lys Gln Arg Arg
 26 50 55 60
 27 Ile Gln Pro Val His Ile Leu Thr Ser Val Ser Ser Leu Arg Gly Thr
 28 65 70 75 80
 29 Arg Glu Cys Ser Val Thr Ser Asp Leu Asp Phe Pro Thr Gln Val Ile
 30 85 90 95
 31 Pro Leu Lys Thr Leu Asn Ala Val Ala Ser Val Pro Ile Met Tyr Ser
 32 100 105 110
 33 Trp Ser Pro Leu Gln Gln Asn Phe Met Val Glu Asp Glu Thr Val Leu
 34 115 120 125
 35 His Asn Ile Pro Tyr Met Gly Asp Glu Val Leu Asp Gln Asp Gly Thr
 36 130 135 140
 37 Phe Ile Glu Glu Leu Ile Lys Asn Tyr Asp Gly Lys Val His Gly Asp
 38 145 150 155 160
 39 Arg Glu Cys Gly Phe Ile Asn Asp Glu Ile Phe Val Glu Leu Val Asn
 40 165 170 175
 41 Ala Leu Gly Gln Tyr Asn Asp Asp Asp Asp Asp Asp Asp Gly Asp Asp
 42 180 185 190
 43 Pro Glu Glu Arg Glu Glu Lys Gln Lys Asp Leu Glu Asp His Arg Asp
 44 195 200 205
 45 Asp Lys Glu Ser Arg Pro Pro Arg Lys Phe Pro Ser Asp Lys Ile Phe
 46 210 215 220
 47 Glu Ala Ile Ser Ser Met Phe Pro Asp Lys Gly Thr Ala Glu Glu Leu
 48 225 230 235 240

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49 Lys Glu Lys Tyr Lys Glu Leu Thr Glu Gln Gln Leu Pro Gly Ala Leu
50                245                250                255
51 Pro Pro Glu Cys Thr Pro Asn Ile Asp Gly Pro Asn Ala Lys Ser Val
52                260                265                270
53 Gln Arg Glu Gln Ser Leu His Ser Phe His Thr Leu Phe Cys Arg Arg
54                275                280                285
55 Cys Phe Lys Tyr Asp Cys Phe Leu His Arg Lys Cys Asn Tyr Ser Phe
56                290                295                300
57 His Ala Thr Pro Asn Thr Tyr Lys Arg Lys Asn Thr Glu Thr Ala Leu
58 305                310                315                320
59 Asp Asn Lys Pro Cys Gly Pro Gln Cys Tyr Gln His Leu Glu Gly Ala
60                325                330                335
61 Lys Glu Phe Ala Ala Ala Leu Thr Ala Glu Arg Ile Lys Thr Pro Pro
62                340                345                350
63 Lys Arg Pro Gly Gly Arg Arg Arg Gly Arg Leu Pro Asn Asn Ser Ser
64                355                360                365
65 Arg Pro Ser Thr Pro Thr Ile Asn Val Leu Glu Ser Lys Asp Thr Asp
66                370                375                380
67 Ser Asp Arg Glu Ala Gly Thr Glu Thr Gly Gly Glu Asn Asn Asp Lys
68 385                390                395                400
69 Glu Glu Glu Glu Lys Lys Asp Glu Thr Ser Ser Ser Ser Glu Ala Asn
70                405                410                415
71 Ser Arg Cys Gln Thr Pro Ile Lys Met Lys Pro Asn Ile Glu Pro Pro
72                420                425                430
73 Glu Asn Val Glu Trp Ser Gly Ala Glu Ala Ser Met Phe Arg Val Leu
74                435                440                445
75 Ile Gly Thr Tyr Tyr Asp Asn Phe Cys Ala Ile Ala Arg Leu Ile Gly
76                450                455                460
77 Thr Lys Thr Cys Arg Gln Val Tyr Glu Phe Arg Val Lys Glu Ser Ser
78 465                470                475                480
79 Ile Ile Ala Pro Ala Pro Ala Glu Asp Val Asp Thr Pro Pro Arg Lys
80                485                490                495
81 Lys Lys Arg Lys His Arg Leu Trp Ala Ala His Cys Arg Lys Ile Gln
82                500                505                510
83 Leu Lys Lys Asp Gly Ser Ser Asn His Val Tyr Asn Tyr Gln Pro Cys
84                515                520                525
85 Asp His Pro Arg Gln Pro Cys Asp Ser Ser Cys Pro Cys Val Ile Ala
86                530                535                540
87 Gln Asn Phe Cys Glu Lys Phe Cys Gln Cys Ser Ser Glu Cys Gln Asn
88 545                550                555                560
89 Arg Phe Pro Gly Cys Arg Cys Lys Ala Gln Cys Asn Thr Lys Gln Cys
90                565                570                575
91 Pro Cys Tyr Leu Ala Val Arg Glu Cys Asp Pro Asp Leu Cys Leu Thr
92                580                585                590
93 Cys Gly Ala Ala Asp His Trp Asp Ser Lys Asn Val Ser Cys Lys Asn
94                595                600                605
95 Cys Ser Ile Gln Arg Gly Ser Lys Lys His Leu Leu Leu Ala Pro Ser
96                610                615                620
97 Asp Val Ala Gly Trp Gly Ile Phe Ile Lys Asp Pro Val Gln Lys Asn

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98 625          630          635          640
99 Glu Phe Ile Ser Glu Tyr Cys Gly Glu Ile Ile Ser Gln Asp Glu Ala
100          645          650          655
101 Asp Arg Arg Gly Lys Val Tyr Asp Lys Tyr Met Cys Ser Phe Leu Phe
102          660          665          670
103 Asn Leu Asn Asn Asp Phe Val Val Asp Ala Thr Arg Lys Gly Asn Lys
104          675          680          685
105 Ile Arg Phe Ala Asn His Ser Val Asn Pro Asn Cys Tyr Ala Lys Val
106          690          695          700
107 Met Met Val Asn Gly Asp His Arg Ile Gly Ile Phe Ala Lys Arg Ala
108 705          710          715          720
109 Ile Gln Thr Gly Glu Glu Leu Phe Phe Asp Tyr Arg Tyr Ser Gln Ala
110          725          730          735
111 Asp Ala Leu Lys Tyr Val Gly Ile Glu Arg Glu Met Glu Ile Pro
112          740          745          750
114 <210> SEQ ID NO: 2
115 <211> LENGTH: 2253
116 <212> TYPE: DNA
117 <213> ORGANISM: Human
119 <400> SEQUENCE: 2
120 atgggccaga ctgggaagaa atctgagaag ggaccagttt gttggcgga gcggtgtaaaa 60
121 tcagagtaca tgcgactgag acagctcaag aggttcagac gagctgatga agtaaagagt 120
122 atgttttagt ccaatcgtca gaaaattttg gaaagaacgg aaatcttaaa ccaagaatgg 180
123 aaacagcgaa ggatacagcc tgtgcacatc ctgacttctg tgagctcatt gcgcgggact 240
124 agggagtgtt cgggtgaccag tgacttggat tttccaacac aagtcacccc attaaagact 300
125 ctgaatgcag ttgcttcagt acccataatg tattcttggg cccccctaca gcagaatttt 360
126 atggtggaag atgaaactgt ttacataaac attccttata tgggagatga agtttttagat 420
127 caggatggta ctttcattga agaactaata aaaaattatg atgggaaagt acacggggat 480
128 agagaatgtg ggttttataaa tgatgaaatt tttgtggagt tgggtgaatgc ccttgggtcaa 540
129 tataatgatg atgacgatga tgatgatgga gacgatcctg aagaaagaga agaaaagcag 600
130 aaagatctgg aggatcaccc agatgataaa gaaagccgcc cacctcggaa atttccttct 660
131 gataaaattt ttgaagccat ttcttcaatg tttccagata agggcacagc agaagaacta 720
132 aaggaaaaat ataaagaact caccgaacag cagctcccag gcgcacttcc tcctgaatgt 780
133 accccaaca tagatggacc aaatgctaaa tctgttcaga gagagcaaag cttacactcc 840
134 tttcatacgc ttttctgtag gcgatgtttt aaatatgact gcttcctaca tcgtaagtgc 900
135 aattattctt ttcatgcaac acccaacact tataagcgga agaacacaga aacagctcta 960
136 gacaacaaac cttgtggacc acagtgttac cagcatttgg agggagcaaa ggagtttgct 1020
137 gctgctctca ccgctgagcg gataaagacc ccacaaaaac gtccaggagg ccgcagaaga 1080
138 ggacggcttc ccaataacag tagcaggccc agcaccccca ccattaatgt gctggaatca 1140
139 aaggatacag acagtgatag ggaagcaggg actgaaacgg ggggagagaa caatgataaa 1200
140 gaagaagaag agaagaaaga tgaaacttcg agctcctctg aagcaaattc tcggtgtcaa 1260
141 acaccaataa agatgaagcc aaatattgaa cctcctgaga atgtggagtg gagtgggtgct 1320
142 gaagcctcaa tgttttagagt cctcattggc acttactatg acaatttctg tgccattgct 1380
143 aggttaattg ggacaaaaac atgtagacag gtgtatgagt ttagagtcaa agaatctagc 1440
144 atcatagctc cagctcccgc tgaggatgtg gatactcctc caaggaaaaa gaagaggaaa 1500
145 caccggttgt gggctgcaca ctgcagaaag atacagctga aaaaggacgg ctctctaac 1560
146 catgtttaca actatcaacc ctgtgatcat ccacggcagc cttgtgacag ttcgtgccct 1620
147 tgtgtgatag cacaaaattt ttgtgaaaag ttttgtcaat gtagttcaga gtgtcaaaac 1680
148 cgctttccgg gatgccgctg caaagcacag tgcaacacca agcagtgccg gtgctacctg 1740

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149 gctgtccgag agtgtgaccc tgacctctgt cttacttgtg gagccgctga ccattggggac 1800
150 agtaaaaatg tgtcctgcaa gaactgcagt attcagcggg gctccaaaaa gcatctattg 1860
151 ctggcaccat ctgacgtggc aggctggggg atttttatca aagatcctgt gcagaaaaat 1920
152 gaattcatct cagaatactg tggagagatt atttctcaag atgaagctga cagaagaggg 1980
153 aaagtgtatg ataaatacat gtgcagcttt ctgttcaact tgaacaatga ttttgtggtg 2040
154 gatgcaaccc gcaagggtaa caaaattcgt tttgcaaate attcggtaaa tccaaactgc 2100
155 tatgcaaaaag ttatgatggt taacggtgat cacaggatag gtatttttgc caagagagcc 2160
156 atccagactg gcgaagagct gttttttgat tacagataga gccaggctga tgccctgaag 2220
157 tatgtcggca tcgaaagaga aatggaaate cct 2253
159 <210> SEQ ID NO: 3
160 <211> LENGTH: 2695
161 <212> TYPE: DNA
162 <213> ORGANISM: Human
164 <400> SEQUENCE: 3
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166 acccgggtggg actcagaagg cagtggagcc ccggcggcgg cggcggcggc gcgcgggggc 120
167 gacgcgcggg aacaacgcga gtcggcgcgc gggacgaaga ataatcatgg gccagactgg 180
168 gaagaaatct gagaagggac cagtttgttg gcggaagcgt gtaaaatcag agtacatgcg 240
169 actgagacag ctcaagaggt tcagacgagc tgatgaagta aagagtatgt ttagttccaa 300
170 tcgtcagaaa attttggaaa gaacggaaat cttaaacca gaatggaaac agcgaaggat 360
171 acagcctgtg cacatcctga cttctgtgag ctcatcgcc gggactaggg agtggtcgg 420
172 gaccagtgac ttggattttc caacacaagt catccatta aagactctga atgcagttgc 480
173 ttcagtaccc ataatgtatt cttggtctcc cctacagcag aattttatgg tggagatga 540
174 aactgtttta cataacattc cttatatggg agatgaagtt ttagatcagg atggtacttt 600
175 cattgaagaa ctaataaaaa attatgatgg gaaagtacac ggggatagag aatgtgggtt 660
176 tataaatgat gaaatTTTTT tggagttggt gaatgccctt ggtcaatata atgatgatga 720
177 cgatgatgat gatggagacg atcctgaaga aagagaagaa aagcagaaag atctggagga 780
178 tcaccgagat gataaagaaa gccgccacc tcggaaattt ccttctgata aaatTTTTTga 840
179 agccatttcc tcaatgtttc cagataaggg cacagcagaa gaactaaagg aaaaatataa 900
180 agaactcacc gaacagcagc tcccaggcgc acttcctcct gaatgtaccc ccaacataga 960
181 tggaccaaat gctaaatctg ttcagagaga gcaaagctta cactcctttc atacgctttt 1020
182 ctgtaggcga tgttttaaat atgactgctt cctacatcgt aagtgcaatt attcctttca 1080
183 tgcaacaccc aacacttata agcggaaaga cacagaaaca gctctagaca acaaaccttg 1140
184 tggaccacag tgttaccagc atttggaggg agcaaaggag tttgctgctg ctctcaccgc 1200
185 tgagcggata aagacccac caaaacgtcc aggaggccgc agaagaggac ggcttcccaa 1260
186 taacagtagc aggccagca cccccaccat taatgtgctg gaatcaaagg atacagacag 1320
187 tgatagggaa gcagggactg aaacgggggg agagaacaat gataaagaag aagaagagaa 1380
188 gaaagatgaa acttcgagct cctctgaagc aaattctcgg tgtcaaacac caataaagat 1440
189 gaagccaaat attgaacctc ctgagaatgt ggagtggagt ggtgctgaag cctcaatggt 1500
190 tagagtcttc attggcactt actatgacaa tttctgtgcc attgctaggt taattgggac 1560
191 caaaacatgt agacaggtgt atgagtttag agtcaaagaa tctagcatca tagctccagc 1620
192 tcccgtgag gatgtggata ctctccaag gaaaaagaag aggaaacacc ggttgtgggc 1680
193 tgcacactgc agaaagatac agctgaaaaa ggacggctcc tctaaccatg tttacaacta 1740
194 tcaaccctgt gatcatccac ggcagccttg tgacagttcg tgcccttggt tgatagcaca 1800
195 aaatTTTTTgt gaaaagtttt gtcaatgtag ttcagagtgt caaaaccgct ttccgggatg 1860
196 ccgtgcaaaa gcacagtgc acaccaagca gtgcccgctg tacctggctg tccgagagtg 1920
197 tgacctgac ctctgtctta cttgtggagc cgctgacat tgggacagta aaaatgtgtc 1980
198 ctgcaagaac tgcagtattc agcggggctc caaaaagcat ctattgctgg caccatctga 2040
199 cgtggcaggc tgggggattt ttatcaaaga tcctgtgcag aaaaatgaat tcattctaga 2100

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200 atactgtgga gagattattt ctcaagatga agctgacaga agaggggaaag tgtatgataa 2160
201 atacatgtgc agcttttctgt tcaacttgaa caatgatttt gtggtggatg caaccgcgcaa 2220
202 gggtaacaaa attcgttttg caaatcattc ggtaaatacca aactgctatg caaaagttat 2280
203 gatgggttaac ggtgatcaca ggataggtat ttttgccaag agagccatcc agactggcga 2340
204 agagctgttt tttgattaca gatacagcca ggctgatgcc ctgaagtatg tcggcatcga 2400
205 aagagaaatg gaaatccctt gacatctgct acctcctccc cctcctctg aaacagctgc 2460
206 cttagcttca ggaacctcga gtactgtggg caatttagaa aaagaacatg cagtttgaaa 2520
207 ttctgaattt gcaaagtact gtaagaataa tttatagtaa tgagttttaa aatcaacttt 2580
208 ttattgcctt ctaccagct gcaaagtgtt ttgtaccagt gaatttttgc aataatgcag 2640
209 tatggtacat ttttcaactt tgaataaaga atacttgaac ttgtcaaaaa aaaaa 2695
211 <210> SEQ ID NO: 4
212 <211> LENGTH: 19
213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
217 <223> OTHER INFORMATION: Primer
219 <400> SEQUENCE: 4
220 gcgcgggacg aagaataat 19
222 <210> SEQ ID NO: 5
223 <211> LENGTH: 21
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: Primer
230 <400> SEQUENCE: 5
231 ggggaggagg tagcagatgt c 21
233 <210> SEQ ID NO: 6
234 <211> LENGTH: 18
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
239 <223> OTHER INFORMATION: Primer
241 <400> SEQUENCE: 6
242 caagcagtgc ccgtgcta 18
244 <210> SEQ ID NO: 7
245 <211> LENGTH: 21
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <223> OTHER INFORMATION: Primer
252 <400> SEQUENCE: 7
253 agcggctcca caagtaagac a 21
255 <210> SEQ ID NO: 8
256 <211> LENGTH: 25
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: Probe
263 <400> SEQUENCE: 8

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RAW SEQUENCE LISTING ERROR SUMMARY

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:11,12,13,14

VERIFICATION SUMMARY

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L:8 M:270 C: Current Application Number differs, Replaced Current Application No

L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date